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cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg 170
Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
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acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg 218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
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Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
            50                  55                  60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag      362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
        65                  70                  75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gat      410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp
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tct ttc aca gga ctg gtc aac atc ttg aca gat att aat tgg cga ttc      458
Ser Phe Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe
95                  100                 105                 110

act gga gac ttc acg gca cct gac ctg gtt tgc cga gtg gtc cgc tat      506
Thr Gly Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr
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ttg cag gtt gtg ctg ctc tac gcc tct acc tac gtc ctg gtg tcc ctc      554
Leu Gln Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu Val Ser Leu
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agc ata gac aga tac cat gcc atc gtc tac ccc atg aag ttc ctt caa      602
Ser Ile Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys Phe Leu Gln
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gga gaa aag caa gcc agg gtc ctc att gtg atc gcc tgg agc ctg tct      650
Gly Glu Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser
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Phe Leu Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu
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tcc aac ggt gaa gtg cag tgc tgg gcc ctg tgg cct gac gac tcc tac      746
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Trp Thr Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro
            210                 215                 220

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Leu Thr Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp
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att aaa agc aaa acc tac gaa aca gtg att tcc aac tgc tca gat ggg      890
Ile Lys Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly
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aaa ctg tgc agc agc tat aac cga gga ctc atc tca aag gca aaa atc      938
Lys Leu Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile
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aag gct atc aag tat agc atc atc atc att ctt gcc ttc atc tgc tgt      986
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Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys
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Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu
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cca gac acc cag gag cgt ttc tat gcc tct gtg atc att cag aac ctg     1082
Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu
        305                 310                 315

cca gca ttg aat agt gcc atc aac ccc ctc atc tac tgt gtc ttc agc     1130
Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser
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agc tcc atc tct ttc ccc tgc agg gag caa aga tca cag gat tcc aga     1178
Ser Ser Ile Ser Phe Pro Cys Arg Glu Gln Arg Ser Gln Asp Ser Arg
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atg acg ttc cgg gag aga act gag agg cat gag atg cag att ctg tcc     1226
Met Thr Phe Arg Glu Arg Thr Glu Arg His Glu Met Gln Ile Leu Ser
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Lys Pro Glu Phe Ile
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Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
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Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
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Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
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Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ser Phe
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Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe Thr Gly
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Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr Leu Gln
        115                 120                 125

Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu Val Ser Leu Ser Ile
    130                 135                 140

Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys Phe Leu Gln Gly Glu
145                 150                 155                 160

Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe Leu
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Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser Asn
            180                 185                 190

Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp Thr
        195                 200                 205

Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr
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Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp Ile Lys
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Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu
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Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile Lys Ala
            260                 265                 270

Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys Trp Ser
        275                 280                 285
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Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu Pro Asp
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Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu Pro Ala
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Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser Ser Ser
325 330 335

Ile Ser Phe Pro Cys Arg Glu Gln Arg Ser Gln Asp Ser Arg Met Thr
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Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
1 5 10

acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg 218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15 20 25 30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac 266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
35 40 45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt 314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe

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aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gat      410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp
    80                  85                  90

tct ttc aca gga ctg gtc aac atc ttg aca gat att aat tgg cga ttc      458
Ser Phe Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe
95                  100                 105                 110

act gga gac ttc acg gca cct gac ctg gtt tgc cga gtg gtc cgc tat      506
Thr Gly Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr
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ttg cag gtt gtg ctg ctc tac gcc tct acc tac gtc ctg gtg tcc ctc      554
Leu Gln Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu Val Ser Leu
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agc ata gac aga tac cat gcc atc gtc tac ccc atg aag ttc ctt caa      602
Ser Ile Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys Phe Leu Gln
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gga gaa aag caa gcc agg gtc ctc att gtg atc gcc tgg agc ctg tct      650
Gly Glu Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser
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ttt ctg ttc tcc att ccc acc ctg atc ata ttt ggg aag agg aca ctg      698
Phe Leu Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu
175                 180                 185                 190

tcc aac ggt gaa gtg cag tgc tgg gcc ctg tgg cct gac gac tcc tac      746
Ser Asn Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr
                195                 200                 205

tgg acc cca tac atg acc atc gtg gcc ttc ctg gtg tac ttc atc cct      794
Trp Thr Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro
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ctg aca atc atc agc atc atg tat ggc att gtg atc cga act att tgg      842
Leu Thr Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp
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att aaa agc aaa acc tac gaa aca gtg att tcc aac tgc tca gat ggg      890
Ile Lys Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly
    240                 245                 250

aaa ctg tgc agc agc tat aac cga gga ctc atc tca aag gca aaa atc      938
Lys Leu Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile
255                 260                 265                 270

aag gct atc aag tat agc atc atc atc att ctt gcc ttc atc tgc tgt      986
Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys
                275                 280                 285

tgg agt cca tac ttc ctg ttt gac att ttg gac aat ttc aac ctc ctt     1034
Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu
            290                 295                 300
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cca gac acc cag gag cgt ttc tat gcc tct gtg atc att cag aac ctg      1082
Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu
        305                 310                 315

cca gca ttg aat agt gcc atc aac ccc ctc atc tac tgt gtc ttc agc      1130
Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser
    320                 325                 330

agc tcc atc tct ttc ccc tgc agg gtc atc cgt ctc cgt cag ctc cag      1178
Ser Ser Ile Ser Phe Pro Cys Arg Val Ile Arg Leu Arg Gln Leu Gln
335                 340                 345                 350

gag gct gcg cta atg ctc tgc cct caa cga gag aac tgg aag ggt act      1226
Glu Ala Ala Leu Met Leu Cys Pro Gln Arg Glu Asn Trp Lys Gly Thr
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Trp Pro Gly Val Pro Ser Trp Ala Leu Pro Arg
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Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
        35                  40                  45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
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Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65                  70                  75                  80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ser Phe
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85 90 95

Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe Thr Gly
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Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr Leu Gln
115 120 125

Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu Val Ser Leu Ser Ile
130 135 140

Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys Phe Leu Gln Gly Glu
145 150 155 160

Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe Leu
165 170 175

Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser Asn
180 185 190

Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp Thr
195 200 205

Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr
210 215 220

Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp Ile Lys
225 230 235 240

Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu
245 250 255

Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile Lys Ala
260 265 270

Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys Trp Ser
275 280 285

Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu Pro Asp
290 295 300

Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu Pro Ala
305 310 315 320

Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser Ser Ser
325 330 335

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Ile Ser Phe Pro Cys Arg Val Ile Arg Leu Arg Gln Leu Gln Glu Ala
            340                 345                 350

Ala Leu Met Leu Cys Pro Gln Arg Glu Asn Trp Lys Gly Thr Trp Pro
        355                 360                 365

Gly Val Pro Ser Trp Ala Leu Pro Arg
    370                 375
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<210> 6

<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(1226)

<400> 6

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ggaggcaagc tggactccct cactcagctg caggagcaag gacagtgagg ctcaaccccg     120

cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg      170
         Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
         1               5                   10

acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg      218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15                  20                  25                  30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac      266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
                35                  40                  45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt      314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
            50                  55                  60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag      362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
        65                  70                  75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gat      410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp
    80                  85                  90
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att aat tgg cga ttc act gga gac ttc acg gca cct gac ctg gtt tgc      458
Ile Asn Trp Arg Phe Thr Gly Asp Phe Thr Ala Pro Asp Leu Val Cys
95                  100                 105                 110

cga gtg gtc cgc tat ttg cag gtt gtg ctg ctc tac gcc tct acc tac      506
Arg Val Val Arg Tyr Leu Gln Val Val Leu Leu Tyr Ala Ser Thr Tyr
                115                 120                 125

gtc ctg gtg tcc ctc agc ata gac aga tac cat gcc atc gtc tac ccc      554
Val Leu Val Ser Leu Ser Ile Asp Arg Tyr His Ala Ile Val Tyr Pro
            130                 135                 140

atg aag ttc ctt caa gga gaa aag caa gcc agg gtc ctc att gtg atc      602
Met Lys Phe Leu Gln Gly Glu Lys Gln Ala Arg Val Leu Ile Val Ile
        145                 150                 155

gcc tgg agc ctg tct ttt ctg ttc tcc att ccc acc ctg atc ata ttt      650
Ala Trp Ser Leu Ser Phe Leu Phe Ser Ile Pro Thr Leu Ile Ile Phe
    160                 165                 170

ggg aag agg aca ctg tcc aac ggt gaa gtg cag tgc tgg gcc ctg tgg      698
Gly Lys Arg Thr Leu Ser Asn Gly Glu Val Gln Cys Trp Ala Leu Trp
175                 180                 185                 190

cct gac gac tcc tac tgg acc cca tac atg acc atc gtg gcc ttc ctg      746
Pro Asp Asp Ser Tyr Trp Thr Pro Tyr Met Thr Ile Val Ala Phe Leu
                195                 200                 205

gtg tac ttc atc cct ctg aca atc atc agc atc atg tat ggc att gtg      794
Val Tyr Phe Ile Pro Leu Thr Ile Ile Ser Ile Met Tyr Gly Ile Val
            210                 215                 220

atc cga act att tgg att aaa agc aaa acc tac gaa aca gtg att tcc      842
Ile Arg Thr Ile Trp Ile Lys Ser Lys Thr Tyr Glu Thr Val Ile Ser
        225                 230                 235

aac tgc tca gat ggg aaa ctg tgc agc agc tat aac cga gga ctc atc      890
Asn Cys Ser Asp Gly Lys Leu Cys Ser Ser Tyr Asn Arg Gly Leu Ile
    240                 245                 250

tca aag gca aaa atc aag gct atc aag tat agc atc atc atc att ctt      938
Ser Lys Ala Lys Ile Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu
255                 260                 265                 270

gcc ttc atc tgc tgt tgg agt cca tac ttc ctg ttt gac att ttg gac      986
Ala Phe Ile Cys Cys Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp
                275                 280                 285

aat ttc aac ctc ctt cca gac acc cag gag cgt ttc tat gcc tct gtg     1034
Asn Phe Asn Leu Leu Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val
            290                 295                 300

atc att cag aac ctg cca gca ttg aat agt gcc atc aac ccc ctc atc     1082
Ile Ile Gln Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile
        305                 310                 315

tac tgt gtc ttc agc agc tcc atc tct ttc ccc tgc agg gtc atc cgt     1130
Tyr Cys Val Phe Ser Ser Ser Ile Ser Phe Pro Cys Arg Val Ile Arg
    320                 325                 330

ctc cgt cag ctc cag gag gct gcg cta atg ctc tgc cct caa cga gag     1178
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Leu Arg Gln Leu Gln Glu Ala Ala Leu Met Leu Cys Pro Gln Arg Glu
335 340 345 350

aac tgg aag ggt act tgg cca ggt gta cct tcc tgg gct ctt cca agg 1226
Asn Trp Lys Gly Thr Trp Pro Gly Val Pro Ser Trp Ala Leu Pro Arg
355 360 365

tgacagctct caccctgtgc tgcaggtggc cctgtgcctg gtgccacttc tcactgctta 1286

ccagggcaca aggacaccag tggttcccaa aatgggtcac agcaggatgg cctgcatcag 1346

attcaccagg gagggctata agaaggcaga c 1377

<210> 7

<211> 366

<212> PRT

<213> Homo sapiens

<400> 7

Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
1 5 10 15

Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
20 25 30

Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
35 40 45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
50 55 60

Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65 70 75 80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ile Asn
85 90 95

Trp Arg Phe Thr Gly Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val
100 105 110

Val Arg Tyr Leu Gln Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu
115 120 125

Val Ser Leu Ser Ile Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys
130 135 140

```
Phe Leu Gln Gly Glu Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp
145                 150                 155                 160

Ser Leu Ser Phe Leu Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys
                165                 170                 175

Arg Thr Leu Ser Asn Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp
            180                 185                 190

Asp Ser Tyr Trp Thr Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr
        195                 200                 205

Phe Ile Pro Leu Thr Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg
    210                 215                 220

Thr Ile Trp Ile Lys Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys
225                 230                 235                 240

Ser Asp Gly Lys Leu Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys
                245                 250                 255

Ala Lys Ile Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe
            260                 265                 270

Ile Cys Cys Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe
        275                 280                 285

Asn Leu Leu Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile
    290                 295                 300

Gln Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys
305                 310                 315                 320

Val Phe Ser Ser Ser Ile Ser Phe Pro Cys Arg Val Ile Arg Leu Arg
                325                 330                 335

Gln Leu Gln Glu Ala Ala Leu Met Leu Cys Pro Gln Arg Glu Asn Trp
            340                 345                 350

Lys Gly Thr Trp Pro Gly Val Pro Ser Trp Ala Leu Pro Arg
        355                 360                 365
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<210> 8

<211> 814

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(410)

<400> 8

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ggaggcaagc tggactccct cactcagctg caggagcaag gacagtgagg ctcaaccccg     120

cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg       170
         Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
         1               5                   10

acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg       218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15                  20                  25                  30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac       266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
                35                  40                  45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt       314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
            50                  55                  60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag       362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
        65                  70                  75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gta       410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Val
    80                  85                  90

taacaagccc acctgcttga gctgggctgc agtggccagg gtaaacatcc aaggcaccag     470

tgaaaaatac agagaaggta aaaggagcaa gagttctgaa gatggaacct gggatggggg     530

aaagtttctt caatctttcc taccaacaag aactccaatt tttcactcct ataaccgtag     590

aagtagaggt aattaggatc atccagcaaa tgcttagagg caaatatccc tggatgagga     650

tgccacagct tattttcatt atatttcttc gattacagtg tggtaatgca tgttgtatgg     710

aactacatat tctttcagaa tgaaaggatt tagaggtggc aagaatatca gcttgaaatt     770

taaagttttt tcataaacaa taaacaaatg ataattgaaa attc                      814
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<210> 9

<211> 94

<212> PRT

<213> Homo sapiens

<400> 9

Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
1 5 10 15

Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
20 25 30

Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
35 40 45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
50 55 60

Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65 70 75 80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Val
85 90

<210> 10

<211> 1463

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(602)

<400> 10
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ggaggcaagc tggactccct cactcagctg caggagcaag gacagtgagg ctcaaccccg 120

cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg 170
Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
1 5 10

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acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg      218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15                  20                  25                  30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac      266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
                35                  40                  45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt      314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
            50                  55                  60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag      362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
        65                  70                  75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca ggt      410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Gly
    80                  85                  90

tgt gct gct cta cgc ctc tac cta cgt cct ggt gtc cct cag cat aga      458
Cys Ala Ala Leu Arg Leu Tyr Leu Arg Pro Gly Val Pro Gln His Arg
95                  100                 105                 110

cag ata cca tgc cat cgt cta ccc cat gaa gtt cct tca agg aga aaa      506
Gln Ile Pro Cys His Arg Leu Pro His Glu Val Pro Ser Arg Arg Lys
                115                 120                 125

gca agc cag ggt cct cat tgt gat cgc ctg gag cct gtc ttt tct gtt      554
Ala Ser Gln Gly Pro His Cys Asp Arg Leu Glu Pro Val Phe Ser Val
            130                 135                 140

ctc cat tcc cac cct gat cat att tgg gaa gag gac act gtc caa cgg      602
Leu His Ser His Pro Asp His Ile Trp Glu Glu Asp Thr Val Gln Arg
        145                 150                 155

tgaagtgcag tgctgggccc tgtggcctga cgactcctac tggaccccat acatgaccat    662

cgtggccttc ctggtgtact tcatccctct gacaatcatc agcatcatgt atggcattgt    722

gatccgaact atttggatta aaagcaaaac ctacgaaaca gtgatttcca actgctcaga    782

tgggaaactg tgcagcagct ataaccgagg actcatctca aaggcaaaaa tcaaggctat    842

caagtatagc atcatcatca ttcttgcctt catctgctgt tggagtccat acttcctgtt    902

tgacattttg gacaatttca acctccttcc agacacccag gagcgtttct atgcctctgt    962

gatcattcag aacctgccag cattgaatag tgccatcaac cccctcatct actgtgtctt   1022

cagcagctcc atctctttcc cctgcaggga gcaaagatca caggattcca gaatgacgtt   1082

ccgggagaga actgagaggc atgagatgca gattctgtcc aagccagaat tcatctagac   1142

cctagggcag tgccagtgct aggctgagca ccatcagctc tcccaggtcc ttgtcacctg   1202

cttgggcacg tgcatggaac ccgagccaac ttcaccccac cctcgtcatt acctgggaga   1262

tgcacaagac aaatgttcta atgactgcat gcactgctta agtattggcc aacacgaact   1322

ccccagttat tcatgccagc caggaaggaa acgccttcct tccccaccat tcccagccct   1382
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ccttcccact ggccagcacc tgaacccagt gaacacaggc attagtggtc cagggtcctg 1442

gcttggagcc agtgagtaga c 1463

<210> 11

<211> 158

<212> PRT

<213> Homo sapiens

<400> 11

Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
1 5 10 15

Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
20 25 30

Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
35 40 45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
50 55 60

Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65 70 75 80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Gly Cys Ala
85 90 95

Ala Leu Arg Leu Tyr Leu Arg Pro Gly Val Pro Gln His Arg Gln Ile
100 105 110

Pro Cys His Arg Leu Pro His Glu Val Pro Ser Arg Arg Lys Ala Ser
115 120 125

Gln Gly Pro His Cys Asp Arg Leu Glu Pro Val Phe Ser Val Leu His
130 135 140

Ser His Pro Asp His Ile Trp Glu Glu Asp Thr Val Gln Arg
145 150 155

<210> 12

<211> 1473

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(536)

<400> 12

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ggaggcaagc tggactccct cactcagctg caggagcaag gacagtgagg ctcaaccccg    120

cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg      170
         Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
         1               5                   10

acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg      218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15                  20                  25                  30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac      266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
                35                  40                  45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt      314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
            50                  55                  60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag      362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
        65                  70                  75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gat      410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp
    80                  85                  90

tct ttc aca gga ctg gtc aac atc ttg aca gat att aat tgg cga ttc      458
Ser Phe Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe
95                  100                 105                 110

act gga gac ttc acg gca cct gac ctg gtt tgc cga gtg gtc cgc tat      506
Thr Gly Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr
                115                 120                 125

ttg cag aaa agc aag cca ggg tcc tca ttg tgatcgcctg gagcctgtct        556
Leu Gln Lys Ser Lys Pro Gly Ser Ser Leu
            130                 135

tttctgttct ccattcccac cctgatcata tttgggaaga ggacactgtc caacggtgaa    616

gtgcagtgct gggccctgtg gcctgacgac tcctactgga ccccatacat gaccatcgtg    676
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gccttcctgg tgtacttcat ccctctgaca atcatcagca tcatgtatgg cattgtgatc 736

cgaactattt ggattaaaag caaaacctac gaaacagtga tttccaactg ctcagatggg 796

aaactgtgca gcagctataa ccgaggactc atctcaaagg caaaaatcaa ggctatcaag 856

tatagcatca tcatcattct tgccttcatc tgctgttgga gtccatactt cctgtttgac 916

attttggaca atttcaacct ccttccagac acccaggagc gtttctatgc ctctgtgatc 976

attcagaacc tgccagcatt gaatagtgcc atcaaccccc tcatctactg tgtcttcagc 1036

agctccatct ctttcccctg cagggagcaa agatcacagg attccagaat gacgttccgg 1096

gagagaactg agaggcatga gatgcagatt ctgtccaagc cagaattcat ctagacccta 1156

gggcagtgcc agtgctaggc tgagcaccat cagctctccc aggtccttgt cacctgcttg 1216

ggcacgtgca tggaacccga gccaacttca ccccaccctc gtcattacct gggagatgca 1276

caagacaaat gttctaatga ctgcatgcac tgcttaagta ttggccaaca cgaactcccc 1336

agttattcat gccagccagg aaggaaacgc cttccttccc caccattccc agccctcctt 1396

cccactggcc agcacctgaa cccagtgaac acaggcatta gtggtccagg gtcctggctt 1456

ggagccagtg agtagac 1473

<210> 13

<211> 136

<212> PRT

<213> Homo sapiens

<400> 13

Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
1 5 10 15

Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
20 25 30

Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
35 40 45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
50 55 60

Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65 70 75 80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ser Phe
85 90 95

Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe Thr Gly
100 105 110

Asp Phe Thr Ala Pro Asp Leu Val Cys Arg Val Val Arg Tyr Leu Gln
115 120 125

Lys Ser Lys Pro Gly Ser Ser Leu
130 135

<210> 14

<211> 1369

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(1043)

<400> 14
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ggaggcaagc tggactccct cactcagctg caggagcaag gacagtgagg ctcaaccccg 120

cctgagcc atg cca gcc aac ttc aca gag ggc agc ttc gat tcc agt ggg 170
Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly
1 5 10

acc ggg cag acg ctg gat tct tcc cca gtg gct tgc act gaa aca gtg 218
Thr Gly Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val
15 20 25 30

act ttt act gaa gtg gtg gaa gga aag gaa tgg ggt tcc ttc tac tac 266
Thr Phe Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr
35 40 45

tcc ttt aag act gag caa ttg ata act ctg tgg gtc ctc ttt gtt ttt 314
Ser Phe Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe
50 55 60

acc att gtt gga aac tcc gtt gtg ctt ttt tcc aca tgg agg aga aag 362
Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys
65 70 75

aag aag tca aga atg acc ttc ttt gtg act cag ctg gcc atc aca gaa 410
Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Glu

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    80                  85                  90

aag caa gcc agg gtc ctc att gtg atc gcc tgg agc ctg tct ttt ctg      458
Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe Leu
95                  100                 105                 110

ttc tcc att ccc acc ctg atc ata ttt ggg aag agg aca ctg tcc aac      506
Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser Asn
                115                 120                 125

ggt gaa gtg cag tgc tgg gcc ctg tgg cct gac gac tcc tac tgg acc      554
Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp Thr
            130                 135                 140

cca tac atg acc atc gtg gcc ttc ctg gtg tac ttc atc cct ctg aca      602
Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr
        145                 150                 155

atc atc agc atc atg tat ggc att gtg atc cga act att tgg att aaa      650
Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp Ile Lys
    160                 165                 170

agc aaa acc tac gaa aca gtg att tcc aac tgc tca gat ggg aaa ctg      698
Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu
175                 180                 185                 190

tgc agc agc tat aac cga gga ctc atc tca aag gca aaa atc aag gct      746
Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile Lys Ala
                195                 200                 205

atc aag tat agc atc atc atc att ctt gcc ttc atc tgc tgt tgg agt      794
Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys Trp Ser
            210                 215                 220

cca tac ttc ctg ttt gac att ttg gac aat ttc aac ctc ctt cca gac      842
Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu Pro Asp
        225                 230                 235

acc cag gag cgt ttc tat gcc tct gtg atc att cag aac ctg cca gca      890
Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu Pro Ala
    240                 245                 250

ttg aat agt gcc atc aac ccc ctc atc tac tgt gtc ttc agc agc tcc      938
Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser Ser Ser
255                 260                 265                 270

atc tct ttc ccc tgc agg gag caa aga tca cag gat tcc aga atg acg      986
Ile Ser Phe Pro Cys Arg Glu Gln Arg Ser Gln Asp Ser Arg Met Thr
                275                 280                 285

ttc cgg gag aga act gag agg cat gag atg cag att ctg tcc aag cca     1034
Phe Arg Glu Arg Thr Glu Arg His Glu Met Gln Ile Leu Ser Lys Pro
            290                 295                 300

gaa ttc atc tagaccctag ggcagtgcca gtgctaggct gagcaccatc             1083
Glu Phe Ile
        305

agctctccca ggtccttgtc acctgcttgg gcacgtgcat ggaacccgag ccaacttcac   1143

cccaccctcg tcattacctg ggagatgcac aagacaaatg ttctaatgac tgcatgcact   1203
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gcttaagtat tggccaacac gaactcccca gttattcatg ccagccagga aggaaacgcc 1263

ttccttcccc accattccca gccctccttc ccactggcca gcacctgaac ccagtgaaca 1323

caggcattag tggtccaggg tcctggcttg gagccagtga gtagac 1369

<210> 15

<211> 305

<212> PRT

<213> Homo sapiens

<400> 15

Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
1 5 10 15

Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
20 25 30

Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
35 40 45

Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
50 55 60

Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
65 70 75 80

Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Glu Lys Gln
85 90 95

Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe Leu Phe Ser
100 105 110

Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser Asn Gly Glu
115 120 125

Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp Thr Pro Tyr
130 135 140

Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr Ile Ile
145 150 155 160

Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp Ile Lys Ser Lys

165 170 175

Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu Cys Ser
180 185 190

Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile Lys Ala Ile Lys
195 200 205

Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile Cys Cys Trp Ser Pro Tyr
210 215 220

Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn Leu Leu Pro Asp Thr Gln
225 230 235 240

Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln Asn Leu Pro Ala Leu Asn
245 250 255

Ser Ala Ile Asn Pro Leu Ile Tyr Cys Val Phe Ser Ser Ser Ile Ser
260 265 270

Phe Pro Cys Arg Glu Gln Arg Ser Gln Asp Ser Arg Met Thr Phe Arg
275 280 285

Glu Arg Thr Glu Arg His Glu Met Gln Ile Leu Ser Lys Pro Glu Phe
290 295 300

Ile
305

<210> 16

<211> 1532

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (231)..(383)

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accatgcctg ccccttata cttgctgttc atagaattgc aactgaaagt gaccatgagg 120

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atccactgga tggagttact tctttcttaa gtgaggaggc taagatctgg agtgacttct    180

ccccagattt ttgtatacct gactctgttt cagcatccgc ttcccaaaga atg cag       236
                                                        Met Gln
                                                        1

tgt gaa gca gga gct tat gtg aga aga aac gca ggg aga cag ttc agt       284
Cys Glu Ala Gly Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln Phe Ser
        5                   10                  15

cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga aaa caa gag       332
His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys Gln Glu
    20                  25                  30

ctc caa tct gtt aga tgg tat ttt gaa gca ggt ctt tgg gta aag gac       380
Leu Gln Ser Val Arg Trp Tyr Phe Glu Ala Gly Leu Trp Val Lys Asp
35                  40                  45                  50

acc tagacccagt gaaggtcatg gtgattatta ttggacaatg ggacatcact            433
Thr

ctgctatttg aacaaataag actttttcct gacatgcatc tggaggcagg tcaaagctcc    493

aggccaactc caagtttctg atggggtctc tagccaatgg aaggcttctt ctccttcaat    553

tgcctgactc ttcaggactc ttaaatactg caaagtgaga aaatgagaca ggttgcactg    613

agggctgtta gccagacaga gtctcgaact ggaagtccat ctagatgttt tgcataagag    673

aatggaaaca atctgtctgt gatttaggga catactctgg cagcaatatg ggaatacagt    733

ttcaatcctc attaacaaaa caggtatgaa atacatattt atttagtaag gtgccagctg    793

tatgaaaaat ccatttctta tttcccataa tgtttctgaa atgtcttagc agtgcataga    853

gacagcatgt catcattttc tagggactgt gtgttattgc atttttccta gggaagatct    913

tttctaggtc acctgctcct tcgctaaagc tctgaccaat ctagcttgct aacctgtgac    973

tccattttcc taagtcctga gagagaaaaa cgctttgcag caaattatgc caggcatcct   1033

tgtgtctaaa tgaaaaaagg aaaaagcctc cttccttccc tctgttgaga agtgcacggt   1093

ccacatatgc atgcacagca tatactgtga gggtatttgc agtcccttgg gttgctttga   1153

taactggcca ggttgctgtt ctatttttcc acattctatt aatcctccta caggcagtta   1213

ttaggtattg agtgctcaca cacccctggc atagtcacca catgccatta gctccagata   1273

aacttccaga aaaaagtcca tcccccactt ctctcagctg cctgccaacg ctggacacct   1333

tctcaccaag ccagcaggac agagaaaagc ctgggcttta agatcaaaca aacacagctt   1393

caaattagga ctctgtcact tcctgtgtac tgggcacttt gctgagtatg tggtttctca   1453

tctgtaaaac agagaaagat gattatctcc caatctttct atgttatatg tttgaattaa   1513

ataaggtact ctccatgaa                                               1532
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<210> 17

<211> 51

<212> PRT

<213> Homo sapiens

<400> 17

Met Gln Cys Glu Ala Gly Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln
1 5 10 15

Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

Gln Glu Leu Gln Ser Val Arg Trp Tyr Phe Glu Ala Gly Leu Trp Val
35 40 45

Lys Asp Thr
50

<210> 18

<211> 1407

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (244)..(402)

<400> 18
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accatgcctg ccccttata cttgctgttc atagaattgc aactgaaagt gaccatgagg 120

atccactgga tggagttact tctttcttaa gtgaggaggc taagatctga gttcttcaca 180

tctctctgta gataaaattt ccggtctggt ttcacattcc tctgtcagaa gaactttctt 240

taa tgt ttc tta aag tac agg tct gct gct tat gtg aga aga aac gca 288
Cys Phe Leu Lys Tyr Arg Ser Ala Ala Tyr Val Arg Arg Asn Ala
1 5 10 15

ggg aga cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg 336

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Gly Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val
                20                  25                  30

aga aga aaa caa gag ctc caa tct gtt aga tgg tat ttt gaa gca ggt      384
Arg Arg Lys Gln Glu Leu Gln Ser Val Arg Trp Tyr Phe Glu Ala Gly
            35                  40                  45

ctt tgg gta aag gac acc tagacccagt gaaggtcatg gtgattatta            432
Leu Trp Val Lys Asp Thr
        50

ttggacaatg ggacatcact ctgctattaa gtgagaaaat gagacaggtt gcactgaggg    492

ctgttagcca gacagagtct cgaactggaa gtccatctag atgttttgca taagagaatg    552

gaaacaatct gtctgtgatt tagggacata ctctggcagc aatatgggaa tacagtttca    612

atcctcatta acaaaacagg tatgaaatac atatttattt agtaaggtgc cagctgtatg    672

aaaaatccat ttcttatttc ccataatgtt tctgaaatgt cttagcagtg catagagaca    732

gcatgtcatc attttctagg gactgtgtgt tattgcattt ttcctaggga agatcttttc    792

taggtcacct gctccttcgc taaagctctg accaatctag cttgctaacc tgtgactcca    852

ttttcctaag tcctgagaga gaaaaacgct ttgcagcaaa ttatgccagg catccttgtg    912

tctaaatgaa aaaaggaaaa agcctccttc cttccctctg ttgagaagtg cacggtccac    972

atatgcatgc acagcatata ctgtgagggt atttgcagtc ccttgggttg ctttgataac   1032

tggccaggtt gctgttctat ttttccacat tctattaatc ctcctacagg cagttattag   1092

gtattgagtg ctcacacacc cctggcatag tcaccacatg ccattagctc cagataaact   1152

tccagaaaaa agtccatccc ccacttctct cagctgcctg ccaacgctgg acaccttctc   1212

accaagccag caggacagag aaaagcctgg gctttaagat caaacaaaca cagcttcaaa   1272

ttaggactct gtcacttcct gtgtactggg cactttgctg agtatgtggt ttctcatctg   1332

taaaacagag aaagatgatt atctcccaat ctttctatgt tatatgtttg aattaaataa   1392

ggtactctcc atgaa                                                    1407
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<210> 19

<211> 53

<212> PRT

<213> Homo sapiens

<400> 19

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Cys Phe Leu Lys Tyr Arg Ser Ala Ala Tyr Val Arg Arg Asn Ala Gly
1               5                   10                  15
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Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
20 25 30

Arg Lys Gln Glu Leu Gln Ser Val Arg Trp Tyr Phe Glu Ala Gly Leu
35 40 45

Trp Val Lys Asp Thr
50

<210> 20

<211> 341

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146)..(328)

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agactttggg ggactactgg aaaggagtga cttctcccca gatttttgta tacctgactc 120

tgtttcagca tccgcttccc aaaga atg cag tgt gaa gca gga gct tat gtg 172
Met Gln Cys Glu Ala Gly Ala Tyr Val
1 5

aga aga aac gca ggg aga cag ttc agt cac tgc aat ctt cat gcc cat 220
Arg Arg Asn Ala Gly Arg Gln Phe Ser His Cys Asn Leu His Ala His
10 15 20 25

cag ttt ctt gtg aga aga aaa caa gtg gat ata cac tgt tcc aag cag 268
Gln Phe Leu Val Arg Arg Lys Gln Val Asp Ile His Cys Ser Lys Gln
30 35 40

cat gtg ttg aaa aga ttt gtc ttt tcc cca ttt aat ggt ctt ggt acc 316
His Val Leu Lys Arg Phe Val Phe Ser Pro Phe Asn Gly Leu Gly Thr
45 50 55

ttt ctc aaa aat tgaccatata tga 341
Phe Leu Lys Asn
60

<210> 21

<211> 61

<212> PRT

<213> Homo sapiens

<400> 21

Met Gln Cys Glu Ala Gly Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln
1 5 10 15

Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

Gln Val Asp Ile His Cys Ser Lys Gln His Val Leu Lys Arg Phe Val
35 40 45

Phe Ser Pro Phe Asn Gly Leu Gly Thr Phe Leu Lys Asn
50 55 60

<210> 22

<211> 710

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(291)

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aaagtgccta ccacatgcta accactgctg caggcacttt ctatagaaga actaatttaa 120

tcatcaccat aaccctatgg ggtagatgat atttttacaa cctccatttt acag atg 177
Met
1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga 225
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
5 10 15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga 273
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
20 25 30

aaa caa gaa aac aag gac tgaaatccac acaggaaggt ggcagtgaac 321
Lys Gln Glu Asn Lys Asp

35

tccacagacg gacctggacg cctcaacact cctggcctta cctcccttgc tgaacgtctc 381

aagtttctct gcgttcagga ctggcaacgc ctgcttcctc ctctgagctg tcaagtagga 441

agtccgggct gctctgctag aaagagaagt catgtgcagg agcactgagg catcccaggt 501

gtgacactct tccacctaga gcattccgtc tctcatcctc tgccatgtga cgctgggctt 561

ctttaacaaa ttaatcccaa gtgcaagaca tttatttctt ctgtacctaa tgacctgagc 621

aatccttctc tgctgaacct ggtagtgtca tctttagaag tgaagacaca attaacacat 681

ggtcatttct tcattatatc gttgttact 710

<210> 23

<211> 39

<212> PRT

<213> Homo sapiens

<400> 23

Met Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly
1 5 10 15

Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
20 25 30

Arg Lys Gln Glu Asn Lys Asp
35

<210> 24

<211> 949

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(366)

<400> 24
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aaagtgccta ccacatgcta accactgctg caggcacttt ctatagaaga actaatttaa 120

tcatcaccat aaccctatgg ggtagatgat atttttacaa cctccatttt acag atg 177
Met
1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga 225
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
5 10 15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga 273
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
20 25 30

aaa caa gac tgg caa cgc ctg ctt cct cct ctg agc tgt caa gta gga 321
Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly
35 40 45

agt ccg ggc tgc tct gct aga aag aga agt cat gtg cag gag cac 366
Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60

tgaggcatcc caggtgtgac actcttccac ctagagcatt ccgtctctca tcctctgcca 426

tgtagcaaac tgctatgcat ccttcagctg caagggattg aatgctatca acaaccatac 486

aagtggagaa gcagatgctt ccctagctga gcctcaggct ttttgatgga attgctacaa 546

cttggtgcat gcctgctcct aaaagaaata ctcaggaatt gtctcataaa gtcctcacct 606

actggcaaaa acaagatgtt ctactcccag gttgactttt tcaagcccca agatgttgag 666

tcagccattc tccaaggatc tcgatttcct tttaatggaa aataacatta aacaccaaat 726

ataagcctcg ctgtcccaca tgcgtattgg ggacaagatg aaacctgctt ccaggctact 786

ttggcagcag aactgaaaaa ggctttttt ccagatatat gatttctcat cgacagggtt 846

gcacagccct ctttattgtt cgtgtaaatg acacccttgg atctgaacaa tacacaccag 906

gacaattgtg tgcaacagtt ctacaaactg atatttctaa tta 949

<210> 25

<211> 64

<212> PRT

<213> Homo sapiens

<400> 25

Met Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly
1 5 10 15

Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg

20 25 30

Arg Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val
35 40 45

Gly Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60

<210> 26

<211> 1068

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(367)

<400> 26

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caaagtgcct accacatgct aaccactgct gcaggcactt tctatagaag aactaattta 120

atcatcacca taaccctatg gggtagatga tatttttaca acctccattt tacag atg 178
Met
1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga 226
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
5 10 15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga 274
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
20 25 30

aaa caa gac tgg caa cgc ctg ctt cct cct ctg agc tgt caa gta gga 322
Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly
35 40 45

agt ccg ggc tgc tct gct aga aag aga agt cat gtg cag gag cac 367
Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60

tgaggcatcc caggtgtgac actcttccac ctagagcatt ccgtctctca tcctctgcca 427

tgtagcaaac tgctatgcat ccttcagctg caagggattg aatgctatca acaaccatac 487

aagtggagaa gcagatgctt ccctagctga gcctcagctc tgttttcctc agtcctaggg 547

gcagattcta atttggtaca gaaaaaaaaa gtactcctgc caattcccat cctggaatga 607

ctgaagaaaa gaaaatgcat gtgattattt taaaggcttt ttgatggaat tgctacaact 667

tggtgcatgc ctgctcctaa aagaaatact caggaattgt ctcataaagt cctcacctac 727

tggcaaaaac aagatgttct actcccaggt tgacttttc aagccccaag atgttgagtc 787

agccattctc caaggatctc gatttccttt taatggaaaa taacattaaa caccaaatat 847

aagcctcgct gtcccacatg cgtattgggg acaagatgaa acctgcttcc aggctacttt 907

ggcagcagaa ctgaaaaagg ctttttttcc agatatatga tttctcatcg acagggttgc 967

acagccctct ttattgttcg tgtaaatgac acccttggat ctgaacaata cacaccagga 1027

caattgtgtg caacagttct acaaactgat atttctaatt a 1068

<210> 27

<211> 64

<212> PRT

<213> Homo sapiens

<400> 27

Met Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly
1 5 10 15

Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
20 25 30

Arg Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val
35 40 45

Gly Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60

<210> 28

<211> 799

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(363)

<400> 28
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aaagtgccta ccacatgcta accactgctg caggcacttt ctatagaaga actaatttaa 120

tcatcaccat aaccctatgg ggtagatgat atttttacaa cctccatttt acag atg 177
Met
1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga 225
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
5 10 15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga 273
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
20 25 30

aaa caa agc aaa ctg cta tgc atc ctt cag ctg caa ggg att gaa tgc 321
Lys Gln Ser Lys Leu Leu Cys Ile Leu Gln Leu Gln Gly Ile Glu Cys
35 40 45

tat caa caa cca tac aag tgg aga agc aga tgc ttc cct agc 363
Tyr Gln Gln Pro Tyr Lys Trp Arg Ser Arg Cys Phe Pro Ser
50 55 60

tgagcctcag gctttttgat ggaattgcta caacttggtg catgcctgct cctaaaagaa 423

atactcagga attgtctcat aaagtcctca cctactggca aaaacaagat gttctactcc 483

caggttgact ttttcaagcc ccaagatgtt gagtcagcca ttctccaagg atctcgattt 543

ccttttaatg gaaaataaca ttaaacacca aatataagcc tcgctgtccc acatgcgtat 603

tggggacaag atgaaacctg cttccaggct actttggcag cagaactgaa aaaggctttt 663

tttccagata tatgatttct catcgacagg gttgcacagc cctctttatt gttcgtgtaa 723

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ctgatatttc taatta 799

<210> 29

<211> 63

<212> PRT

<213> Homo sapiens

<400> 29

Met Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly
1 5 10 15

Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
20 25 30

Arg Lys Gln Ser Lys Leu Leu Cys Ile Leu Gln Leu Gln Gly Ile Glu
35 40 45

Cys Tyr Gln Gln Pro Tyr Lys Trp Arg Ser Arg Cys Phe Pro Ser
50 55 60

<210> 30

<211> 834

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(251)

<400> 30

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Met Pro Leu Asp Leu Met Leu Glu
1 5

aga ctt aag act ttg ggg gac tac tgg aaa gct tat gtg aga aga aac 101
Arg Leu Lys Thr Leu Gly Asp Tyr Trp Lys Ala Tyr Val Arg Arg Asn
10 15 20

gca ggg aga cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt 149
Ala Gly Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu
25 30 35 40

gtg aga aga aaa caa gac tgg caa cgc ctg ctt cct cct ctg agc tgt 197
Val Arg Arg Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys
45 50 55

caa gta gga agt ccg ggc tgc tct gct aga aag aga agt cat gtg cag 245
Gln Val Gly Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln
60 65 70

gag cac tgaggcatcc caggtgtgac actcttccac ctagagcatt ccgtctctca 301
Glu His

tcctctgcca tgtagcaaac tgctatgcat ccttcagctg caagggattg aatgctatca 361

acaaccatac aagtggagaa gcagatgctt ccctagctga gcctcaggct ttttgatgga 421

attgctacaa cttggtgcat gcctgctcct aaaagaaata ctcaggaatt gtctcataaa 481

gtcctcacct actggcaaaa acaagatgtt ctactcccag gttgactttt tcaagcccca 541

agatgttgag tcagccattc tccaaggatc tcgatttcct tttaatggaa aataacatta 601

aacaccaaat ataagcctcg ctgtcccaca tgcgtattgg ggacaagatg aaacctgctt 661

ccaggctact ttggcagcag aactgaaaaa ggctttttt ccagatatat gatttctcat 721

cgacagggtt gcacagccct ctttattgtt cgtgtaaatg acacccttgg atctgaacaa 781

tacacaccag gacaattgtg tgcaacagtt ctacaaactg atatttctaa tta 834

<210> 31

<211> 74

<212> PRT

<213> Homo sapiens

<400> 31

Met Pro Leu Asp Leu Met Leu Glu Arg Leu Lys Thr Leu Gly Asp Tyr
1 5 10 15

Trp Lys Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln Phe Ser His Cys
20 25 30

Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys Gln Asp Trp Gln
35 40 45

Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly Ser Pro Gly Cys Ser
50 55 60

Ala Arg Lys Arg Ser His Val Gln Glu His
65 70

<210> 32

<211> 550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(366)

<400> 32

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tcatcaccat aaccctatgg ggtagatgat atttttacaa cctccatttt acag atg        177
                                                              Met
                                                               1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga        225
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
            5                  10                  15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga        273
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
        20                  25                  30

aaa caa gac tgg caa cgc ctg ctt cct cct ctg agc tgt caa gta gga        321
Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly
    35                  40                  45

agt ccg ggc tgc tct gct aga aag aga agt cat gtg cag gag cac            366
Ser Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50                  55                  60

tgaggcatcc caggtgtgac actcttccac ctagagcatt ccgtctctca tcctctgcca     426

tgtgccatgt tttgaaccac tagattagag ggtcaagcaa tttcttggaa ttttactctg     486

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Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
            20                  25                  30

Arg Lys Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val
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tcatcaccat aaccctatgg ggtagatgat atttttacaa cctccatttt acag atg 177
Met
1

aag aaa ctg aag cat aga cct gct tat gtg aga aga aac gca ggg aga 225
Lys Lys Leu Lys His Arg Pro Ala Tyr Val Arg Arg Asn Ala Gly Arg
5 10 15

cag ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga 273
Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg
20 25 30

aaa caa gtg gat ata cac tgt tcc aag cag cat gtg ttg aaa aga ttt 321
Lys Gln Val Asp Ile His Cys Ser Lys Gln His Val Leu Lys Arg Phe
35 40 45

gtc ttt tcc cca ttt aat ggt ctt ggt acc ttt ctc aaa aat 363
Val Phe Ser Pro Phe Asn Gly Leu Gly Thr Phe Leu Lys Asn
50 55 60

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Arg Gln Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg
20 25 30

Arg Lys Gln Val Asp Ile His Cys Ser Lys Gln His Val Leu Lys Arg
35 40 45

Phe Val Phe Ser Pro Phe Asn Gly Leu Gly Thr Phe Leu Lys Asn
50 55 60

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<212> DNA

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tgtttcagca tccgcttccc aaaga atg cag tgt gaa gca gga gct tat gtg 172
Met Gln Cys Glu Ala Gly Ala Tyr Val
1 5

aga aga aac gca ggg aga cag ttc agt cac tgc aat ctt cat gcc cat 220
Arg Arg Asn Ala Gly Arg Gln Phe Ser His Cys Asn Leu His Ala His
10 15 20 25

cag ttt ctt gtg aga aga aaa caa gtt taggaaaact tcctacacct 267
Gln Phe Leu Val Arg Arg Lys Gln Val
30

tctttgttgg gatgttctct ggactaatga ctccaggcga gaccaccgtt gatcatgaac 327

tcactttgaa acagaagctg ggttggtaag actggagcta ct 369

<210> 37

<211> 34

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Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
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Gln Val

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Met Gln Cys Glu Ala Gly Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln
1 5 10 15

ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga aaa 157
Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

caa gaa aac aag gac tgaaatccac acaggaaggt ggcagtgaac tccacagacg 212
Gln Glu Asn Lys Asp
35

gacctggacg cctcaacact cctggcctta cctcccttgc tgaacgtctc aagtttctct 272

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tggccctacc agaaaaagga aatgatttga atgtgcgcca aaaaatatgt tttctttctt 452

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Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

Gln Glu Asn Lys Asp
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Met Gln Cys Glu Ala Gly Ala Tyr Val Arg Arg Asn Ala Gly Arg Gln
1 5 10 15

ttc agt cac tgc aat ctt cat gcc cat cag ttt ctt gtg aga aga aaa 157
Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

caa gac tgg caa cgc ctg ctt cct cct ctg agc tgt caa gta gga agt 205
Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly Ser
35 40 45

ccg ggc tgc tct gct aga aag aga agt cat gtg cag gag cac 247
Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60

tgaggcatcc caggtgtgac actcttccac ctagagcatt ccgtctctca tcctctgcca 307

tgtagcaaac tgctatgcat ccttcagctg caagggattg aatgctatca acaaccatac 367

aagtggagaa gcagatgctt ccctagctga gcctcaggct ttttgatgga attgctacaa 427

cttggtgcat gcctgctcct aaaagaaata ctcaggaatt gtctcataaa gtcctcacct 487

actggcaaaa acaagatgtt ctactcccag gttgactttt tcaagcccca agatgttgag 547

tcagccattc tccaaggatc tcgatttcct tttaatggaa aataacatta aacaccaaat 607

ataagcctcg ctgtcccaca tgcgtattgg ggacaagatg aaacctgctt ccaggctact 667

ttggcagcag aactgaaaaa ggctttttt ccagatatat gatttctcat cgacagggtt 727

gcacagccct ctttattgtt cgtgtaaatg acacccttgg atctgaacaa tacacaccag 787

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Phe Ser His Cys Asn Leu His Ala His Gln Phe Leu Val Arg Arg Lys
20 25 30

Gln Asp Trp Gln Arg Leu Leu Pro Pro Leu Ser Cys Gln Val Gly Ser
35 40 45

Pro Gly Cys Ser Ala Arg Lys Arg Ser His Val Gln Glu His
50 55 60